Editorials

Light at the End of the Tunnel?

IN AN ADDRESS BEFORE a recent meeting of the American Bar Association in San Francisco, Lee Iacocca, Chairman of the Chrysler Corporation, is reported (*San Francisco Chronicle,* Aug 11, 1987, p1,22) to have referred to litigious lawyers as "Public Enemy No. One," and he then went on to say that the number of product liability suits rose 1,000% during the period 1975 to 1985 and the amount of jury awards doubled during this time. He was further reported as stating that although cars get safer every day, automobiles account for half of all the injury suits filed and half of the awards, and that Americans are spending $30 billion a year suing each other and thus creating a climate that discourages risk taking in business, which is all important to success and even survival in a competitive world. He noted that "other countries don't spend their time looking for Mr. Deep Pockets" and called attention to the number of lawyers we have in this country by suggesting that "Japan has about as many lawyers as we have sumo wrestlers."

In medicine it is professional liability more than product liability that is the problem, but the parallels are obvious enough, and many physicians would agree that a litigious public, aided and abetted by litigious lawyers, is indeed "Public Enemy No. One," and that lawsuits and the threat of lawsuits seriously interfere with professional judgment and the taking of reasonable risks that are just as essential in patient care as they are in a competitive business such as automobile manufacturing. In both, the current epidemic of litigation has a paralyzing effect on the day to day conduct of practice or business that is not in the ultimate interest of either patients or the public. And this is not to mention the costs in dollars and human resources when these are spent in expensive, time-consuming legal confrontations that only add costly heat and friction to economic systems already under strain, again whether it be automobile manufacturing or patient care. It is all too sad, but all too true, that the most certain beneficiaries of this wave of human litigiousness are the lawyers who feed, and often feed quite handsomely, off it, as Mr Iacocca pointed out in his reported speech at the American Bar Association meeting.

For quite some time physicians and their patients have been feeling the heat and friction and, in the final analysis, bearing the costs of what has surely become excessive litigiousness in health care. As an inevitable consequence, physicians and lawyers are finding themselves in open confrontation with one another, whether in the courts or in legislative arenas, and it is worth noting that these confrontations are always on the lawyers' turf and are always conducted under rules of the game that are basically determined by lawyers.

Perhaps one can take heart, however. There may be a reason for hope. When someone of Lee Iacocca's prestige and stature in the business and industrial world calls the spade of excessive litigation the spade that it is, a new force of responsible public opinion has come upon the scene. With other nonprofessional leaders of similar prestige and stature now coming forth and speaking out in like fashion, it is just possible that we are beginning to see some light at the end of what has seemed to many physicians and many nonphysicians a very long and dismally dark tunnel.

MSMW

The Geneticist's Grail

IN A LECTURE delivered at the Western Association of Physicians meeting in Carmel, California, on February 3, 1987, Dr Ray White and co-workers reviewed and updated the current strategies used in the identification of human genetic loci. They described the recent successes in identifying the disease loci for chronic granulomatous disease, Duchenne muscular dystrophy, cystic fibrosis and retinoblastoma and referred to impending breakthroughs in a number of other diseases such as familial polyposis, ataxia telangiectasia, neurofibromatosis and other muscular dystrophies and neurologic disorders. The localization of a disease-associated gene to a region of the genome is an important first step. Once achieved, a variety of clinical applications and potential benefits can be derived from this information.

Central to the ability to map genes to a particular locus was the advent of recombinant DNA technology, which has enabled investigators to isolate genes. There are two fundamental approaches to gene isolation, depending on whether or not the protein encoded by the gene affected in a particular genetic disorder is known. When the protein has been defined, the strategy for isolating the gene is now quite straightforward. It involves the use of synthetic DNA probes constructed according to the amino acid sequence or antibodies directed against the protein of interest. The probe or antibody is then used to identify the gene that codes for the recognized protein.

A more difficult task confronts investigators who are searching for genetic loci in diseases in which the affected protein is not known and the locus on the human chromosome may or may not be defined. Linkage analysis has enabled scientists recently to map and identify DNA sequences associated with this category of disorders. Successes have included some of the most important genetic conditions that, until now, had proved largely undecipherable by classical analysis—such as neurofibromatosis, cystic fibrosis, Huntington's chorea and Duchenne muscular dystrophy. The strategy for locating these genes depends on the use of DNA polymorphisms. Within the human genome are frequent variations or polymorphisms in DNA sequences, many of which are neutral. A variety of different polymorphisms exists. One type is caused by a single nucleotide change in the DNA that either creates a restriction endonuclease cleavage site or abolishes an existing one. Digesting DNA from different persons with the appropriate enzyme generates fragments of two discrete lengths according to the presence or absence of a restriction site.

Another type of DNA fragment length variation is due to tandem repeats of short nucleotide sequences that occur in many regions throughout the human genome. The function of these tandem repeats is not known, but the number of repeats in a region differs from person to person. Therefore, digesting DNA with the appropriate enzyme generates polymorphic fragments of different lengths due to the differing number of repeats. Because of the large number of variations possible in the number of repeat sequences present, instead of a two-allele system, a highly informative multiallele system results.[1,2] Each parental chromosome can then be distinguished and used to trace the inheritance of the particular segment of the genome.